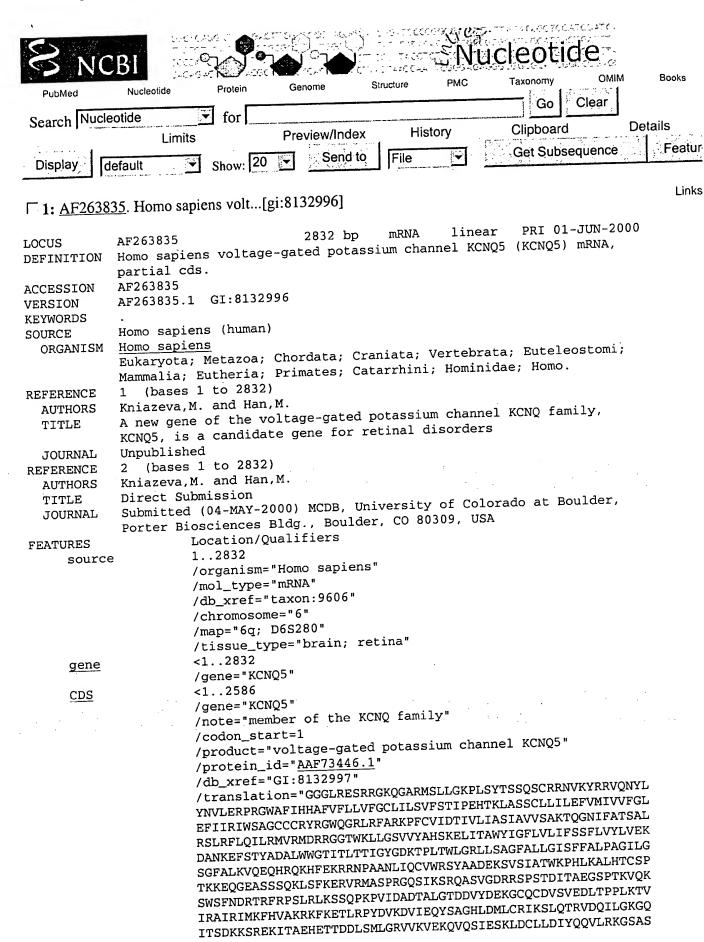
>AF263835 ACCESSION:AF263835 NID: gi 8132996 gb AF263835.1 AF263835 Homo sapiens voltage-gated potassium channel KCNQ5 (KCNQ5) mRNA, partial cds Length = 2832

Score = 1688 bits (4323), Expect = 0.0 Identities = 846/861 (98%), Positives = 849/861 (98%), Gaps = 9/861 (1%) Frame = +1Query: 72 GGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHA 131 GGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFI+HA GGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIHHA 180 Sbjct: 1 Query: 132 FVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGW 191 FVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGW Sbjct: 181 FVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGW 360 Query: 192 QGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGT 251 QGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGT Sbjct: 361 QGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGT 540 Query: 252 WKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTT 311 WKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTT Sbjct: 541 WKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTT 720 Query: 312 IGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAA 371 IGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAA Sbjct: 721 IGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAA 900 Query: 372 NLIQCVWRSYAADEKSVSIATWKPHLKALHTCSPT-----NQKLSFKERVRMASPR 422 NLIQCVWRSYAADEKSVSIATWKPHLKALHTCSPT +OKLSFKERVRMASPR Sbjct: 901 NLIQCVWRSYAADEKSVSIATWKPHLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPR 1080 Query: 423 GQSIKSRQASVGDRRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDAD 482 GQSIKSRQASVGDRRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDAD Sbjct: 1081GQSIKSRQASVGDRRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDAD 1260 Query: 483 TALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIE 542 TALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIE Sbjct: 1261TALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIE 1440 Query: 543 QYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEK 602 QYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEK Sbjct: 1441QYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEK 1620 Query: 603 QVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQ 662 QVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQ Sbjct: 1621QVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQ 1800 Query: 663 NSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNT 722 NSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQSDGSAV ATNT Sbjct: 1801NSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQSDGSAVVATNT 1980 Query: 723 IANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQESISDVTTCLVASKENV 782 IANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQESISDVTTCLVASKENV Sbjct: 1981IANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQESISDVTTCLVASKENV 2160 Query: 783 QVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSES QVAQSNL KDRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSES Sbjct: 2161QVAQSNLPKDRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSES 2340

Query: 843 SGSRGSQDFYPKWRESKLFITDEEVGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSS 902
SGSRG QDFYPKWRESKLFITDEEVGPEETETDTFDAAPQPAREAAFASDSLRTGRS+SS Sbjct: 2341SGSRGRQDFYPKWRESKLFITDEEVGPEETETDTFDAAPQPAREAAFASDSLRTGRSQSS 2520

Query: 903 QSICKAGESTDALSLPHVKLK 923 QSICKAGESTDALSLPHVKLK Sbjct: 2521QSICKAGESTDALSLPHVKLK 2583



2821 cctgagaaac ca

11

ALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN EFSAQTFYALSPTMHSQATQVPISQSDGSAVVATNTIANQINTAPKPAAPTTLQIPPP LPAIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLPKDRSMRKSFDMG GETLLSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGRQDFYPKWRESKL FITDEEVGPEETETDTFDAAPQPAREAAFASDSLRTGRSQSSQSICKAGESTDALSLP HVKLK"

701 t 663 g 685 c BASE COUNT 783 a ORIGIN 1 ggcggtggcc tgagggagag ccgccggggc aagcaggggg cccggatgag cctgctgggg 61 aagccgctct cttacacgag tagccagagc tgccggcgca acgtcaagta ccggcgggtg 121 cagaactacc tgtacaacgt gctggagaga ccccgcggct gggcgttcat ccaccacgct 181 ttcgtttttc tccttgtctt tggttgcttg attttgtcag tgttttctac catccctgag 241 cacacaaaat tggcctcaag ttgcctcttg atcctggagt tcgtgatgat tgtcgtcttt 301 ggtttggagt tcatcattcg aatctggtct gcgggttgct gttgtcgata tagaggatgg 361 caaggaagac tgaggtttgc tcgaaagccc ttttgtgtta tagataccat tgttcttatc 421 gcttcaatag cagttgtttc tgcaaaaact cagggtaata tttttgccac gtctgcactc 481 agaagtetee gttteetaca gateeteege atggtgegea tggaeegaag gggaggeaet 541 tggaaattac tgggttcagt ggtttatgct cacagcaagg aattaatcac agcttggtac 601 ataggatttt tggttcttat tttttcgtct ttccttgtct atctggtgga aaaggatgcc 661 aataaagagt tttctacata tgcagatgct ctctggtggg gcacaattac attgacaact 721 attggctatg gagacaaaac tcccctaact tggctgggaa gattgctttc tgcaggcttt 781 gcactccttg gcatttcttt ctttgcactt cctgccggca ttcttggctc aggttttgca 841 ttaaaagtac aagaacaaca ccgccagaaa cactttgaga aaagaaggaa cccagctgcc 901 aacctcattc agtgtgtttg gcgtagttac gcagctgatg agaaatctgt ttccattgca 961 acctggaagc cacacttgaa ggccttgcac acctgcagcc ctaccaagaa agaacaaggg 1021 gaagcatcaa gcagtcagaa gctaagtttt aaggagcgag tgcgcatggc tagccccagg 1081 ggccagagta ttaagagccg acaagcctca gtaggtgaca ggaggtcccc aagcaccgac 1141 atcacagecg agggeagtee caccaaagtg cagaagaget ggagetteaa egacegaace 1201 cgcttccggc cctcgctgcg cctcaaaagt tctcagccaa aaccagtgat agatgctgac 1261 acagecettg geactgatga tgtatatgat gaaaaaggat gecagtgtga tgtateagtg 1321 gaagacctca ccccaccact taaaactgtc attcgagcta tcagaattat gaaatttcat 1381 gttgcaaaac ggaagtttaa ggaaacatta cgtccatatg atgtaaaaga tgtcattgaa 1441 caatattctg ctggtcatct ggacatgttg tgtagaatta aaagccttca aacacgtgtt 1501 gatcaaattc ttggaaaagg gcaaatcaca tcagataaga agagccgaga gaaaataaca 1561 gcagaacatg agaccacaga cgatctcagt atgctcggtc gggtggtcaa ggttgaaaaa 1621 caggtacagt ccatagaatc caagctggac tgcctactag acatctatca acaggtcctt 1681 cggaaagget etgeeteage ectegetttg getteattee agateceace ttttgaatgt 1741 gaacagacat ctgactatca aagccctgtg gatagcaaag atctttcggg ttccgcacaa 1801 aacagtggct gcttatccag atcaactagt gccaacatct cgagaggcct gcagttcatt 1861 ctgacgccaa atgagttcag tgcccagact ttctacgcgc ttagccctac tatgcacagt 1921 caagcaacac aggtgccaat tagtcaaagc gatggctcag cagtggtagc caccaacacc 1981 attgcaaacc aaataaatac ggcacccaag ccagcagccc caacaacttt acagatccca 2041 cetectetee cagecateaa geatetgeee aggecagaaa etetgeacee taaceetgea 2101 ggcttacagg aaagcatttc tgacgtcacc acctgccttg ttgcctccaa ggaaaatgtt 2161 caggttgcac agtcaaatct acccaaggac cgttctatga ggaaaagctt tgacatggga 2221 ggagaaactc tgttgtctgt ctgtcccatg gtgccgaagg acttgggcaa atctttgtct 2281 gtgcaaaacc tgatcaggtc gaccgaggaa ctgaatatac aactttcagg gagtgagtca 2341 agtggctcca gaggccgcca agatttttac cccaaatgga gggaatccaa attgtttata 2401 actgatgaag aggtgggtcc cgaagagaca gagacagaca cttttgatgc cgcaccgcag 2461 cctgccaggg aagctgcctt tgcatcagac tctctaagga ctggaaggtc acaatcatct 2521 cagagcattt gtaaggcagg agaaagtaca gatgccctca gcttgcctca tgtcaaactg 2581 aaataagttc ttcattttct ttccaggcat agcagttctt tagctataca tatcattgca 2641 tgaactattt cgaaagccct tctaaaaagt tgaaattgca agaatcggga agaacatgaa 2701 aggcagttta taagcccgtt accttttaat tgcatgaaaa tgcatgttta gggatggcta 2761 aaattccaag gtgcatcgac attaacccac tcatttagta atgtaccttg agttaaaaag

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